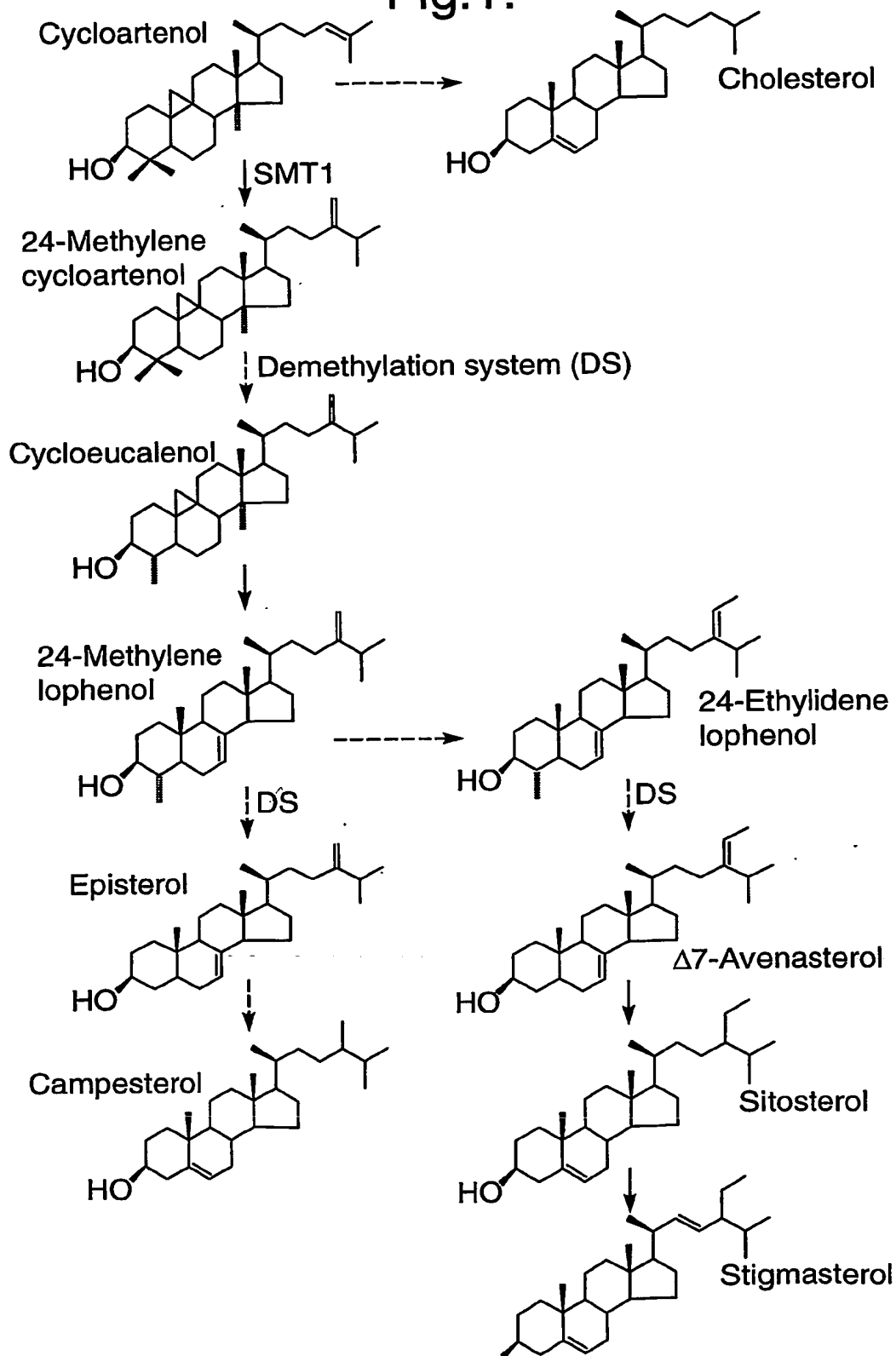


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Fig.1.



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Fig.2.

1 ATGCAGTACC TTGTTACGCA TTTCAGTGAC TTTCAACTGG CGTGTATTGG GAGTTTATA
M Q Y L V T H F S D F Q L A C I G S F I

61 CTTTCATGAAA GCGTGTTTTT CTGTCTGGA CTCCCTTACA TTTTCCTAGA AAGGACTGGT
L H E S V F F L S G L P Y I F L E R T G

121 TTTCTGAGCA ACTACAAAAT TCAGACCAA AGTAATACTC CTGAAGCCCA GGGAAAATGC
F L S N Y K I Q T K S N T P E A Q G K C

181 ATTGCTCGAC TATTACTTTA CCATTGCTGC GTAAACTTGC CCCTCATGAT GGCCTCGTAT
I A R L L L Y H C C V N L P L M M A S Y

241 CCTGTATTCA GATTCATGGG CATGGAAAGC AGTTTTCCTC TGCCGTCCTG GAAAGTGGTG
P V F R F M G M E S S F P L P S W K V V

301 TCTGCCCAGA TCTTATTCTA CTTTCATCATT GAGGATTTTG TATTCTATTG GGGTCACAGG
S A Q I L F Y F I I E D F V F Y W G H R

361 ATCTTGCATA CTAAATGGCT CTACAAGAAC GTGCACAGTG TGCATCATGA GTACGCGACA
I L H T K W L Y K N V H S V H H E Y A T

421 CCGTTTGGTT TGACATCAGA ATATGCTCAT CCCGCTGAAA TTCTGTTTCCT TGGTTTGGCT
P F G L T S E Y A H P A E I L F L G F A

481 ACCATTGTTG GTCCGGCTCT CACCGGGCCT CACCTGATCA CCCTTTGGTT ATGGATGATG
T I V G P A L T G P H L I T L W L W M M

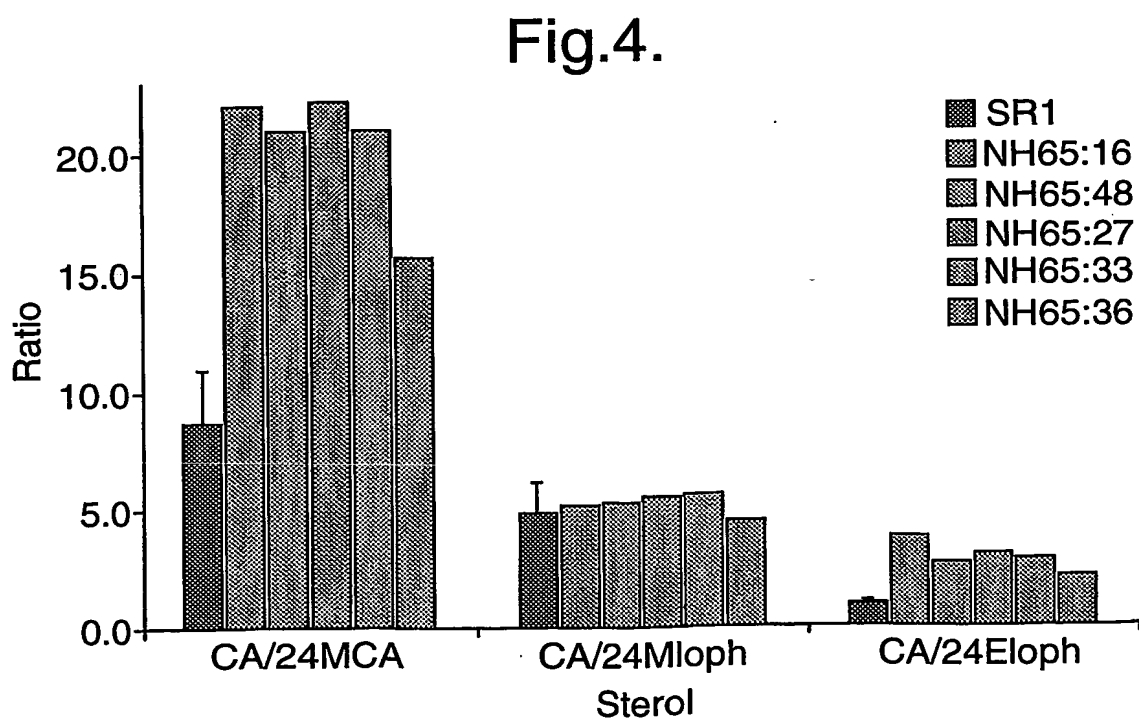
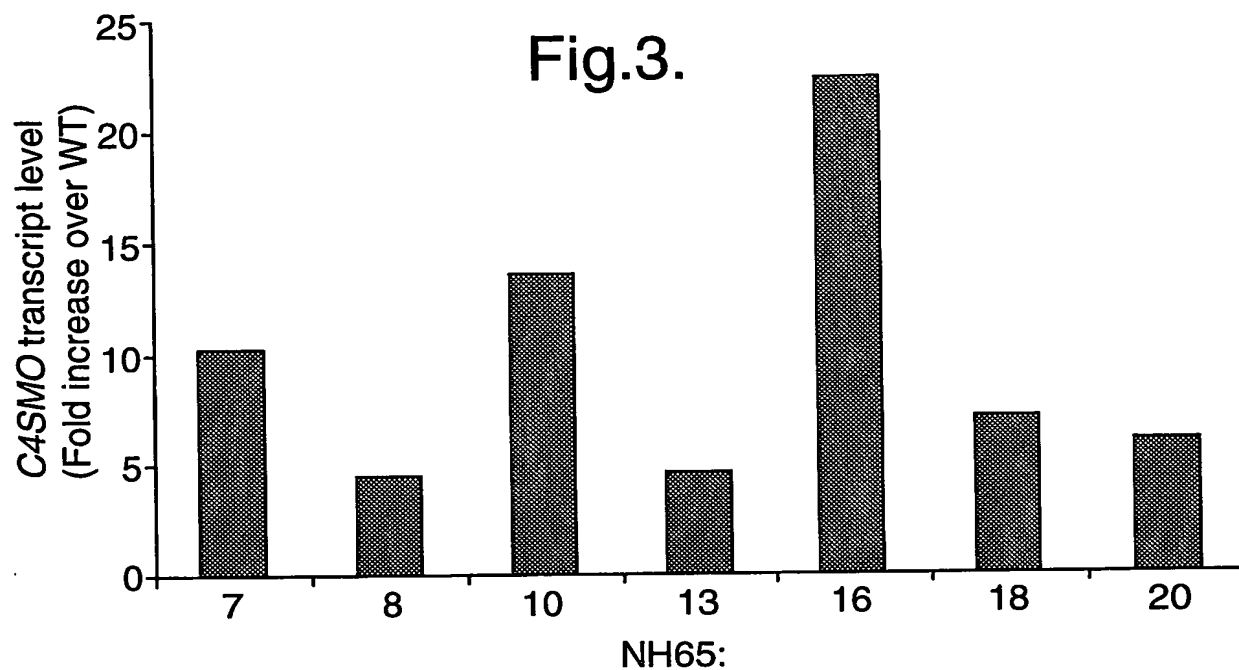
541 CTCAGAGTTA TTGAGACAGT TGAGGCACAT TGTGGTTATC ATTTCCCATG GAGCCCTCG
L R V I E T V E A H C G Y H F P W S P S

601 AATTTTCTTC CTCTATACGG CGGTGCTGAC TTCCATGACT ACCATCATCG ATTACTCTAC
N F L P L Y G G A D F H D Y H H R L L Y

661 ACAAAGTCTG GCAACTACTC ATCAACGTTT GTTTACATGG ACTGGATCTT TGGCACCGAT
T K S G N Y S S T F V Y M D W I F G T D

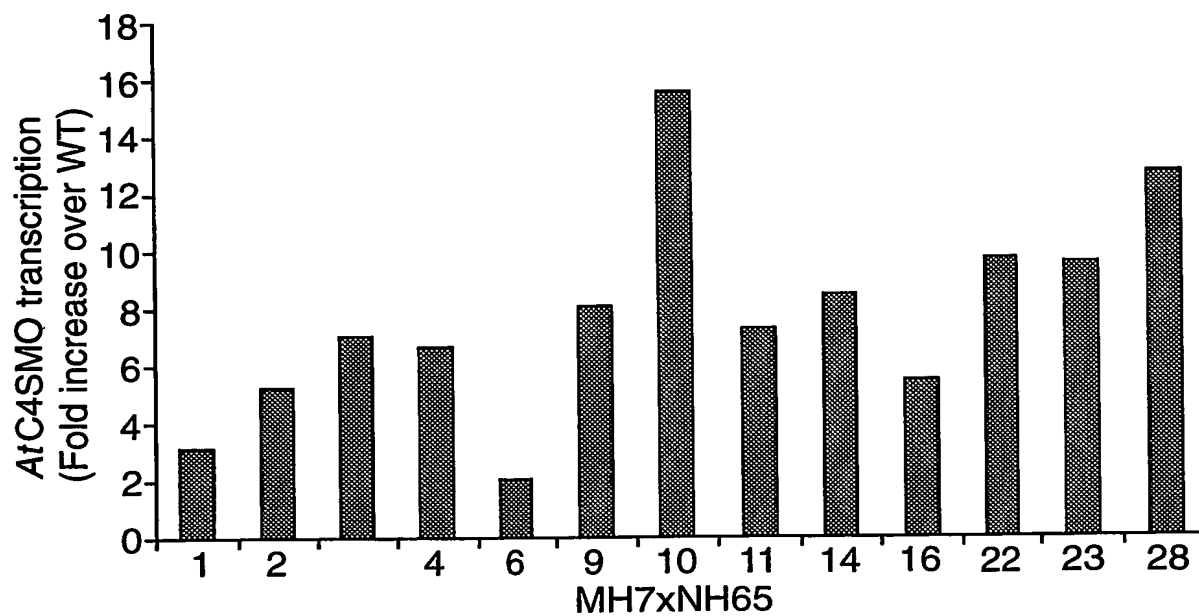
721 AAAGGTTACA GAAAACCTAA GGCCCTAAAA GAAACCTGA
K G Y R K L K A L K E T -

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Fig.5.



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Fig.6A.

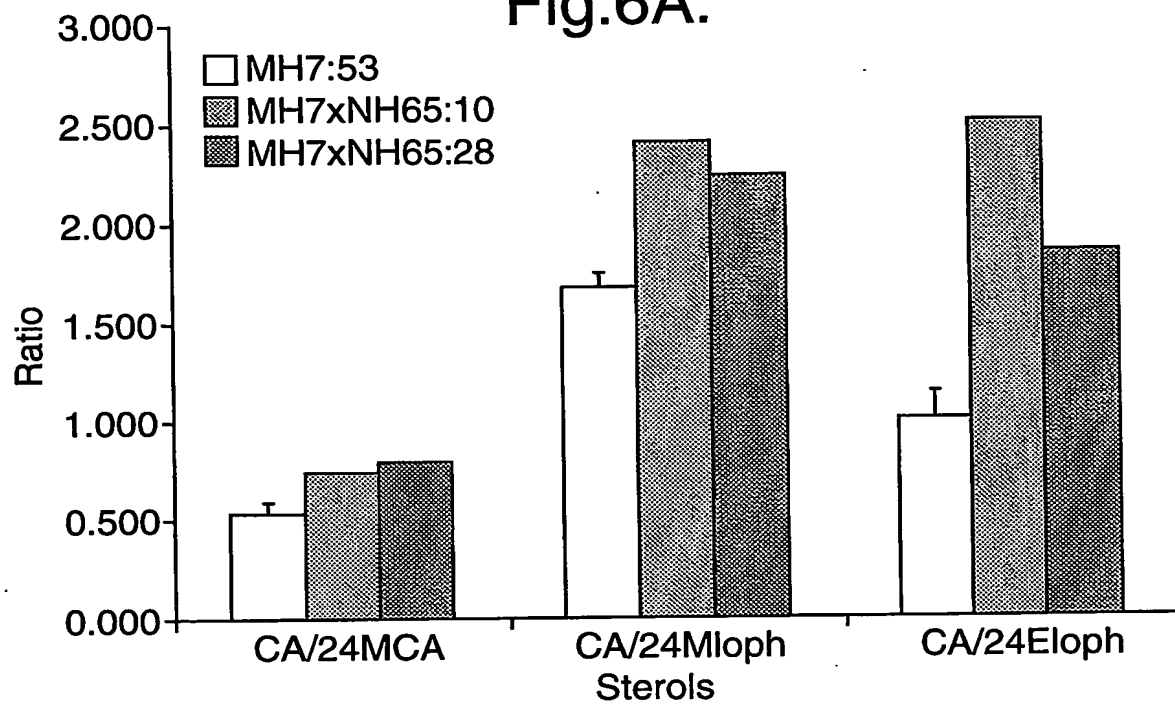


Fig.6B.

